



## SEQUENCE LISTING

<110> Sagami Chemical Research Center, Protegene Inc.

<120> Human proteins having hydrophobic domains and DNAs encoding these proteins

<130> 661924

<140> US/10/019,151

<141> 2003-01-31

<150> JP 11-178065

<151> 1999-06-24

<160> 24

<210> 1

<211> 238

<212> PRT

<213> Homo sapiens

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Val	Met	Pro	Pro	Gln	Phe	Lys	Lys	Asp	Leu	Asp	Ser	Tyr	Leu	Lys	Thr
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Arg	Ser	Pro	Val	Thr	Phe	Leu	Ser	Asp	Leu	Arg	Ser	Asn	Leu	Gln	Val
	50					55				60					
Ser	Asn	Glu	Pro	Gly	Asn	Arg	Tyr	Asn	Leu	Gln	Leu	Ile	Asn	Ala	Leu
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Val	Leu	Tyr	Val	Gly	Thr	Gln	Ala	Ile	Ala	His	Ile	His	Asn	Lys	Gly
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Ser	Thr	Pro	Ser	Met	Ser	Thr	Ile	Thr	His	Ser	Ala	His	Met	Asp	Ile
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Leu	Asn	Ala	Ile	Ala	Asn	Gln	Leu	Arg	Tyr	Pro	Asn	Ser	His	Thr	His
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Tyr	Phe	Ser	Cys	Thr	Met	Leu	Tyr	Leu	Phe	Ala	Glu	Ala	Asn	Thr	Glu
145					150				155					160	
Ala	Ile	Gln	Glu	Gln	Ile	Thr	Arg	Val	Leu	Leu	Glu	Arg	Leu	Ile	Val
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Asn	Arg	Pro	His	Pro	Trp	Gly	Leu	Leu	Ile	Thr	Phe	Ile	Glu	Leu	Ile
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Lys	Asn	Pro	Ala	Phe	Lys	Phe	Trp	Asn	His	Glu	Phe	Val	His	Cys	Ala
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Pro	Glu	Ile	Glu	Lys	Leu	Phe	Gln	Ser	Val	Ala	Gln	Cys	Cys	Met	Gly
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<211> 339

<212> PRT

<213> Homo sapiens

<400> 2

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Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His  
35 40 45  
Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu  
50 55 60  
Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val  
65 70 75 80  
Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu  
85 90 95  
Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val  
100 105 110  
Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly  
115 120 125  
Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln  
130 135 140  
Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp  
145 150 155 160  
Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu  
165 170 175  
Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu  
180 185 190  
Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro  
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Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro  
210 215 220  
Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His  
225 230 235 240  
Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr  
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Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile  
260 265 270  
Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp  
275 280 285  
Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn  
290 295 300  
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<210> 3

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<212> PRT

<213> Homo sapiens

<400> 3

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Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp Met Pro Val Ser  
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Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val Val Gln Tyr Asn

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Trp	Glu	Thr	Gly	Asp	Asp	Arg	Phe	Ser	Phe	Arg	Ser	Phe	Arg	Ser	Gly
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Met	Trp	Leu	Ser	Cys	Glu	Glu	Thr	Val	Glu	Glu	Pro	Gly	Glu	Arg	Cys
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Arg	Ser	Phe	Ile	Glu	Leu	Thr	Pro	Pro	Ala	Lys	Arg	Glu	Ile	Leu	Trp
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Leu	Ser	Leu	Gly	Thr	Gln	Ile	Thr	Tyr	Ile	Gly	Leu	Gln	Phe	Ile	Ser
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Phe	Leu	Leu	Leu	Leu	Thr	Asp	Leu	Leu	Leu	Thr	Gly	Asn	Pro	Ala	Cys
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Gly	Leu	Lys	Leu	Ser	Ala	Phe	Ala	Ala	Val	Ser	Ser	Val	Leu	Ser	Gly
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Leu	Leu	Gly	Met	Val	Ala	His	Met	Met	Tyr	Ser	Gln	Val	Phe	Gln	Ala
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Thr	Val	Asn	Leu	Gly	Pro	Glu	Asp	Trp	Arg	Pro	His	Val	Trp	Asn	Tyr
		195					200					205			
Gly	Trp	Ala	Phe	Tyr	Met	Ala	Trp	Leu	Ser	Phe	Thr	Cys	Cys	Met	Ala
	210					215					220				
Ser	Ala	Val	Thr	Thr	Phe	Asn	Thr	Tyr	Thr	Arg	Met	Val	Leu	Glu	Phe
225					230					235					240
Lys	Cys	Lys	His	Ser	Lys	Ser	Phe	Lys	Glu	Asn	Pro	Asn	Cys	Leu	Pro
			245						250					255	
His	His	His	Gln	Cys	Phe	Pro	Arg	Arg	Leu	Ser	Ser	Ala	Ala	Pro	Thr
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Val	Gly	Pro	Leu	Thr	Ser	Tyr	His	Gln	Tyr	His	Asn	Gln	Pro	Ile	His
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Ser	Val	Ser	Glu	Gly	Val	Asp	Phe	Tyr	Ser	Glu	Leu	Arg	Asn	Lys	Gly
	290					295					300				
Phe	Gln	Arg	Gly	Ala	Ser	Gln	Glu	Leu	Lys	Glu	Ala	Val	Arg	Ser	Ser
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Val	Glu	Glu	Glu	Gln	Cys										
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			20					25					30		
Ala	Gly	Pro	Asp	Glu	Asp	Leu	Ser	His	Arg	Asn	Lys	Glu	Pro	Pro	Ala
		35					40					45			
Pro	Ala	Gln	Gln	Leu	Gln	Pro	Gln	Pro	Val	Ala	Val	Gln	Gly	Pro	Glu
	50					55					60				
Pro	Ala	Arg	Val	Glu	Lys	Ile	Phe	Thr	Pro	Ala	Ala	Pro	Val	His	Thr
	65				70					75				80	
Asn	Lys	Glu	Asp	Pro	Ala	Thr	Gln	Thr	Asn	Leu	Gly	Phe	Ile	His	Ala
			85						90					95	
Phe	Val	Ala	Ala	Ile	Ser	Val	Ile	Ile	Val	Ser	Glu	Leu	Gly	Asp	Lys
			100					105					110		
Thr	Phe	Phe	Ile	Ala	Ala	Ile	Met	Ala	Met	Arg	Tyr	Asn	Arg	Leu	Thr
		115					120					125			
Val	Leu	Ala	Gly	Ala	Met	Leu	Ala	Leu	Gly	Leu	Met	Thr	Cys	Leu	Ser
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145					150					155					160

Tyr	Val	Ser	Thr	Val	Leu	Phe	Ala	Ile	Phe	Gly	Ile	Arg	Met	Leu	Arg
				165					170					175	
Glu	Gly	Leu	Lys	Met	Ser	Pro	Asp	Glu	Gly	Gln	Glu	Glu	Leu	Glu	Glu
			180					185					190		
Val	Gln	Ala	Glu	Leu	Lys	Lys	Lys	Asp	Glu	Glu	Phe	Gln	Arg	Thr	Lys
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Leu	Leu	Asn	Gly	Pro	Gly	Asp	Val	Glu	Thr	Gly	Thr	Ser	Ile	Thr	Val
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Pro	Gln	Lys	Lys	Trp	Leu	His	Phe	Ile	Ser	Pro	Ile	Phe	Val	Gln	Ala
225					230					235					240
Leu	Thr	Leu	Thr	Phe	Leu	Ala	Glu	Trp	Gly	Asp	Arg	Ser	Gln	Leu	Thr
				245					250					255	
Thr	Ile	Val	Leu	Ala	Ala	Arg	Glu	Asp	Pro	Tyr	Gly	Val	Ala	Val	Gly
			260					265					270		
Gly	Thr	Val	Gly	His	Cys	Leu	Cys	Thr	Gly	Leu	Ala	Val	Ile	Gly	Gly
		275					280					285			
Arg	Met	Ile	Ala	Gln	Lys	Ile	Ser	Val	Arg	Thr	Val	Thr	Ile	Ile	Gly
	290					295					300				
Gly	Ile	Val	Phe	Leu	Ala	Phe	Ala	Phe	Ser	Ala	Leu	Phe	Ile	Ser	Pro
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Leu	His	Ile	Val	Leu	Leu	Ser	Ile	Pro	Phe	Val	Ser	Val	Pro	Val	Val
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Trp	Thr	Leu	Thr	Asn	Leu	Ile	His	Asn	Met	Gly	Met	Tyr	Ile	Phe	Leu
	50				55					60					
His	Thr	Val	Lys	Gly	Thr	Pro	Phe	Glu	Thr	Pro	Asp	Gln	Gly	Lys	Ala
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Arg	Leu	Leu	Thr	His	Trp	Glu	Gln	Met	Asp	Tyr	Gly	Val	Gln	Phe	Thr
				85					90					95	
Ala	Ser	Arg	Lys	Phe	Leu	Thr	Ile	Thr	Pro	Ile	Val	Leu	Tyr	Phe	Leu
			100					105					110		
Thr	Ser	Phe	Tyr	Thr	Lys	Tyr	Asp	Gln	Ile	His	Phe	Val	Leu	Asn	Thr
		115				120						125			
Val	Ser	Leu	Met	Ser	Val	Leu	Ile	Pro	Lys	Leu	Pro	Gln	Leu	His	Gly
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145					150										

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Leu	His	Met	Val	Leu	Leu	Ser	Ile	Pro	Phe	Phe	Ser	Ile	Pro	Val	Val

		35				40				45							
Trp	Thr	Leu	Thr	Asn	Val	Ile	His	Asn	Leu	Ala	Thr	Tyr	Val	Phe	Leu		
	50					55					60						
His	Thr	Val	Lys	Gly	Thr	Pro	Phe	Glu	Thr	Pro	Asp	Gln	Gly	Lys	Ala		
	65				70					75					80		
Arg	Leu	Leu	Thr	His	Trp	Glu	Gln	Met	Asp	Tyr	Gly	Leu	Gln	Phe	Thr		
				85					90					95			
Ser	Ser	Arg	Lys	Phe	Leu	Ser	Ile	Ser	Pro	Ile	Val	Leu	Tyr	Leu	Leu		
			100					105					110				
Ala	Ser	Phe	Tyr	Thr	Lys	Tyr	Asp	Ala	Ala	His	Phe	Leu	Ile	Asn	Thr		
		115					120					125					
Ala	Ser	Leu	Leu	Ser	Val	Leu	Leu	Pro	Lys	Leu	Pro	Gln	Phe	His	Gly		
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Val	Arg	Val	Phe	Gly	Ile	Asn	Lys	Tyr									
145					150												

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			20					25					30				
Tyr	Leu	Arg	Lys	Glu	Met	Thr	Gln	Asn	Ile	Tyr	Gln	Met	Ala	Thr	Phe		
		35					40					45					
Gly	Thr	Thr	Ala	Gly	Phe	Ser	Gly	Ile	Phe	Ser	Asn	Phe	Leu	Phe	Arg		
	50				55					60							
Arg	Cys	Phe	Lys	Val	Lys	His	Asp	Ala	Leu	Lys	Thr	Tyr	Ala	Ser	Leu		
	65				70					75				80			
Ala	Thr	Leu	Pro	Phe	Leu	Ser	Thr	Val	Val	Thr	Asp	Lys	Leu	Phe	Val		
				85				90					95				
Ile	Asp	Ala	Leu	Tyr	Ser	Asp	Asn	Ile	Ser	Lys	Glu	Asn	Cys	Val	Phe		
		100					105					110					
Arg	Ser	Ser	Leu	Ile	Gly	Ile	Val	Cys	Gly	Val	Phe	Tyr	Pro	Ser	Ser		
		115				120						125					
Leu	Ala	Phe	Thr	Lys	Asn	Gly	Arg	Leu	Ala	Thr	Lys	Tyr	His	Thr	Val		
	130					135					140						
Pro	Leu	Pro	Pro	Lys	Gly	Arg	Val	Leu	Ile	His	Trp	Met	Thr	Leu	Cys		
	145				150				155					160			
Gln	Thr	Gln	Met	Lys	Leu	Met	Ala	Ile	Pro	Leu	Val	Phe	Gln	Ile	Met		
			165					170					175				
Phe	Gly	Ile	Leu	Asn	Gly	Leu	Tyr	His	Tyr	Ala	Val	Phe	Glu	Glu	Thr		
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Leu	Glu	Lys	Thr	Ile	His	Glu	Glu										
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		20					25					30					
Gln	Leu	Asp	Asp	Glu	Glu	Met	Tyr	Ser	Ala	His	Met	Pro	Ala	His	Leu		



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tcaaaactcag	acacgaaaac	cagaactgca	tcaggatatg	gtggtaccag	gagacga	1017

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 <213> Homo sapiens

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ggcacacaga	aggtgcccaa	gcccctgtgc	gagaaaggtc	tggcagccaa	gtgctttgac	180
atgccagtgt	ccttggtatg	agataccaac	acatccaccc	aggaggtggt	acaatacaac	240
tgggagactg	gggatgaccg	gttctccttc	cggagcttcc	ggagtggcat	gtggctatcc	300
tgtgaggaaa	ctgtggaaga	accaggggag	aggtgccgaa	gtttcattga	acttacacca	360
ccagccaaga	gagaaatcct	atggttatcc	ctgggaacgc	agatcaccta	catcggactt	420
caattcatca	gcttcctcct	gtactaaca	gacttgctac	tcactgggaa	ccctgcctgt	480
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tgtttccctc	ggcggtgtgc	aagtgcagcc	cccacgtggg	gtcctttgac	cagctaccac	840
cagtatcata	atcagcccat	ccactctgtc	tctgagggag	tcgacttcta	ctccgagctg	900
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caccggaaca	aagaaccgcc	ggcgccggcc	cagcagctgc	agccgcagcc	tgtggctgtg	180
cagggccccc	agccggcccc	ggtcgagaaa	atatttacac	cagcagctcc	agttcatacc	240
aataaagaag	atcctgctac	ccaaactaat	ttgggattta	tccatgcatt	tgtcgtgcc	300
atatcagtta	ttattgtatc	tgaattgggt	gataagacat	tttttatagc	agccatcatg	360
gcaatgcgct	ataaccgcct	gaccgtgctg	gctgggtgca	tgcttgccct	gggactaatg	420
acatgcttgt	cagttttgtt	tggtatgccc	accacagtca	tcccaggggt	ctatacatat	480
tatgtttcaa	ctgtattatt	tgccattttt	ggcattagaa	tgcttcggga	aggcttaaag	540
atgagccctg	atgaggggtc	agaggaactg	gaagaagttc	aagctgaatt	aaagaagaaa	600
gatgaagaat	ttcaacgaac	caaactttta	aatggaccgg	gagatgttga	aacgggtaca	660
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gcagctagag aggaccoccta tgggtgtagcc gtgggtggaa ctgtggggca ctgcctgtgc						840
acgggatttg cagtaattgg aggaagaatg atagcacaga aaatctctgt cagaactgtg						900
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ccgtttgtga gtgtccctgt cgtctggacc ctacccaacc tcattcaca catgggcatg 180  
tatatcttcc tgcacacggg gaaggggaca ccctttgaga ccccggaaca gggcaaggcg 240  
aggctgctaa cccactggga gcagatggat tatggggctc agttcacggc ctctcggaag 300  
ttcttgacca tcacacccat cgtgctgtac ttctcacca gcttctacac taagtacgac 360  
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cagctccacg gagtccggat ttttggaaatc aataagtac 459

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cccttcttca gcattcctgt tgtctggacc ctgaccaacg tcattccataa cctggctacg 180  
tatgtcttcc ttcatacggg gaaagggaca ccctttgaga ctctgacca aggaaaggct 240  
cggctactga cacactggga gcaaatggac tatgggctcc agtttacctc ttcccgcaag 300  
ttcctcagca tctctcctat tgtgctctat ctctggcca gcttctatac caagtatgat 360  
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aatatatatc aaatggcgac atttggaaca acagctggtt tctctggaat attctcaaac 180  
ttcctgttca gacgctgctt caagggttaa catgatgctt tgaagacata tgcattcattg 240  
gctacacttc catttttgtc tactgttgtt actgacaagc tttttgtaat tgatgctttg 300  
tattcagata atataagcaa ggaaaactgt gttttcagaa gctcactgat tggcatagtt 360  
tgtgtgtgtt tctatcccag ttctttggct tttactaaaa atggacgcct ggcaaccaag 420  
tatcataccg ttccactgcc accaaaagga agggttttta tccattggat gacgctttgt 480  
caaacacaaa tgaaattaat ggcgattcct ctagtcttcc agattatggt tggaatatta 540  
aatggtctat accattatgc agtatttgaa gagacacttg agaaaactat acatgaagag 600

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<213> Homo sapiens

<400> 16  
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tcagcccaca tgcccgtcga cctgcgctgt gatgcctgca gagctgtggc ttaccagatg 180  
tggcaaaaatc tggcaaggc agagacaaa ctctacac ctcaactctg gggcgggcg 240  
gagctgagcg agttgggtcta cacggatgtc ctggaccgga gctgctcccg gaactggcag 300  
gactacggag ttcgagaagt ggaccaagt aaacgtctca caggcccagg acttagcgag 360  
gggccagagc caagcatcag cgtgatggct acagggggcc cctggcctac caggctctcc 420  
aggacatggt tgcactactt gggggagttt ggagaagacc agatctatga agcccaccaa 480  
caaggccgag gggctctgga ggcattgcta tgtgggggac cccagggggc ctgctcagag 540  
aaggtgtcag ccacaagaga agagctc 567



<210> 17  
 <211> 1167  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (187)...(903)

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 tatagtgtat atagtttttag aaaaacagtc ccaccactta agcatagatg taatttacta 180  
 ataaaa atg att ctg ctt gtg att ctt gca ttt tat ctg tgg cag gtg 228  
 Met Ile Leu Leu Val Ile Leu Ala Phe Tyr Leu Trp Gln Val  
 1 5 10  
 gac atg ttg agt gaa att aac att gct ccc cgg att ctc acc aat ttc 276  
 Asp Met Leu Ser Glu Ile Asn Ile Ala Pro Arg Ile Leu Thr Asn Phe  
 15 20 25 30  
 act gga gta atg cca cct cag ttc aaa aag gat ttg gat tcc tat ctt 324  
 Thr Gly Val Met Pro Gln Phe Lys Lys Asp Leu Asp Ser Tyr Leu  
 35 40 45  
 aaa act cga tca cca gtc act ttc ctg tct gat ctg cgc agc aac cta 372  
 Lys Thr Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu  
 50 55 60  
 cag gca tcc aat gaa cct ggg aat cgc tac aac ctc cag ctc atc aat 420  
 Gln Val Ser Asn Glu Pro Gly Asn Arg Tyr Asn Leu Gln Leu Ile Asn  
 65 70 75  
 gca ctg gtg ctc tat gtc ggg act cag gcc att gcg cac atc cac aac 468  
 Ala Leu Val Leu Tyr Val Gly Thr Gln Ala Ile Ala His Ile His Asn  
 80 85 90  
 aag ggc agc aca cct tca atg agc acc atc act cac tca gca cac atg 516  
 Lys Gly Ser Thr Pro Ser Met Ser Thr Ile Thr His Ser Ala His Met  
 95 100 105 110  
 gat atc ttc cag aat ttg gct gtg gac ttg gac act gag ggt cgc tat 564  
 Asp Ile Phe Gln Asn Leu Ala Val Asp Leu Asp Thr Glu Gly Arg Tyr  
 115 120 125  
 ctc ttt ttg aat gca att gca aat cag ctc cgg tac cca aat agc cac 612  
 Leu Phe Leu Asn Ala Ile Ala Asn Gln Leu Arg Tyr Pro Asn Ser His  
 130 135 140  
 act cac tac ttc agt tgc acc atg ctg tac ctt ttt gca gag gcc aat 660  
 Thr His Tyr Phe Ser Cys Thr Met Leu Tyr Leu Phe Ala Glu Ala Asn  
 145 150 155  
 acg gaa gcc atc caa gaa cag atc aca aga gtt ctc ttg gaa cgg ttg 708  
 Thr Glu Ala Ile Gln Glu Gln Ile Thr Arg Val Leu Leu Glu Arg Leu  
 160 165 170  
 att gta aat agg cca cat cct tgg ggt ctt ctt att acc ttc att gag 756  
 Ile Val Asn Arg Pro His Pro Trp Gly Leu Leu Ile Thr Phe Ile Glu  
 175 180 185 190  
 ctg att aaa aac cca gcg ttt aag ttc tgg aac cat gaa ttt gta cac 804  
 Leu Ile Lys Asn Pro Ala Phe Lys Phe Trp Asn His Glu Phe Val His  
 195 200 205  
 tgt gcc cca gaa atc gaa aag tta ttc cag tcg gtc gca cag tgc tgc 852  
 Cys Ala Pro Glu Ile Glu Lys Leu Phe Gln Ser Val Ala Gln Cys Cys  
 210 215 220  
 atg gga cag aag cag gcc cag caa gta atg gaa ggg aca ggt gcc agt 900  
 Met Gly Gln Lys Gln Ala Gln Gln Val Met Glu Gly Thr Gly Ala Ser  
 225 230 235  
 tagacgaaac tgcattctctg ttgtacgtgt cagtctagag gtctcactgc accgagttca 960  
 taaactgact gaagaatcct ttcagctcct cctgactttc ccagcccttt ggtttgtggg 1020

tatctgcccc aactactgtt gggatcagcc tcctgtctta tgtgggcacg ttccaaagtt 1080  
 taaatgcatt tttttgactc ttggccaaaa tttagaagat gctgtgaata tcattttgaa 1140  
 cttgtgtaaa tacatgaaag agaaaaac 1167

<210> 18  
 <211> 1925  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (115)... (1134)

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 cccagggttcg gcccgtaggc gtctggcagc ccggcgccat cttcatcgag cgcc atg 117  
 Met  
 1  
 gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc 165  
 Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly  
 5 10 15  
 ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac 213  
 Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp  
 20 25 30  
 cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat 261  
 Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr  
 35 40 45  
 gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa 309  
 Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys  
 50 55 60 65  
 tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata 357  
 Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile  
 70 75 80  
 cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt 405  
 Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys  
 85 90 95  
 aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc 453  
 Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser  
 100 105 110  
 tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct 501  
 Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly Ser  
 115 120 125  
 tgt ggc ttg gag tat aat tta gat tat aca gaa ctt ggc ctg cag aaa 549  
 Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys  
 130 135 140 145  
 ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat tat 597  
 Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr  
 150 155 160  
 tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att 645  
 Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile  
 165 170 175  
 acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc 693  
 Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe  
 180 185 190  
 ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca 741  
 Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro  
 195 200 205  
 ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct ccc 789  
 Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro  
 210 215 220 225

cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggr cat ggt 837  
Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly  
230 235 240  
gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa 885  
Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu  
245 250 255  
aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta 933  
Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu  
260 265 270  
gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg 981  
Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser  
275 280 285  
tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg 1029  
Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg  
290 295 300 305  
gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca 1077  
Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser  
310 315 320  
aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg 1125  
Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg  
325 330 335  
aga cga taaagtagaa agttggagtc aaacactgga tgcagaaatt ttggatttt 1180  
Arg Arg

tcatacctttt ctcttttagaa aaaaagtact acctgttaac aattgggaaa aggggatatt 1240  
caaaagtctt gtggtgttat gtccagtgtg gctttttgta ttctattatt tgaggctaaa 1300  
agttgatgtg tgacaaaata cttatgtgtt gtatgtcagt gtaacatgca gatgtatatt 1360  
gcagtttttg aaagtgatca ttactgtgga atgctaaaaa tacattaatt tctaaaacct 1420  
gtgatgccct aagaagcatt aagaatgaag gtgttgact aatagaaact aagtacagaa 1480  
aatttcagtt ttagggtggt gttagctgatg agttattacc tcatagagac tataatattc 1540  
tatttggtat tatattttt gatgtttgct gttcttcaaa catttaaatc aagctttgga 1600  
ctaattatgc taatttgtga gttctgatca cttttgagct ctgaagcttt gaatcattca 1660  
gtggtggaga tggccttctg gtaactgaat attaccttct gtaggaaaag gtggaaaata 1720  
agcatctaga aggttggtgt gaatgactct gtgctggcaa aaatgcttga aacctctata 1780  
tttctttcgt tcataagagg taaaggtcaa atttttcaac aaaagtcttt taataacaaa 1840  
agcatgcagt tctctgtgaa atctcaaata ttgttgtaat agtctgtttc aatcttaaaa 1900  
agaatcaata aaaacaaaca agggg 1925

<210> 19  
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<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (71)...(1051)

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gacgctgacc atg gcc aag atg gag ctc tgg aag gcc ttc tct ggc cag 109  
Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln  
1 5 10  
cgg aca ctc cta tct gcc atc ctc agc atg cta tca ctc agc ttc tcc 157  
Arg Thr Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser  
15 20 25  
aca aca tcc ctg ctc agc aac tac tgg ttt gtg ggc aca cag aag gtg 205  
[Thr Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val  
30 35 40 45  
ccc aag ccc ctg tgc gag aaa ggt ctg gca gcc aag tgc ttt gac atg 253  
Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp Met

	50		55		60	
cca gtg tcc ctg gat gga gat acc aac acā tcc acc cag gag gtg gta						301
Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val Val						
	65		70		75	
caa tac aac tgg gag act ggg gat gac cgg ttc tcc ttc cgg agc ttc						349
Gln Tyr Asn Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe Arg Ser Phe						
	80		85		90	
cgg agt ggc atg tgg cta tcc tgt gag gaa act gtg gaa gaa cca ggg						397
Arg Ser Gly Met Trp Leu Ser Cys Glu Glu Thr Val Glu Glu Pro Gly						
	95		100		105	
gag agg tgc cga agt ttc att gaa ctt aca cca cca gcc aag aga gaa						445
Glu Arg Cys Arg Ser Phe Ile Glu Leu Thr Pro Pro Ala Lys Arg Glu						
	110		115		120	125
atc cta tgg tta tcc ctg gga acg cag atc acc tac atc gga ctt caa						493
Ile Leu Trp Leu Ser Leu Gly Thr Gln Ile Thr Tyr Ile Gly Leu Gln						
	130		135		140	
ttc atc agc ttc ctc ctg cta cta aca gac ttg cta ctc act ggg aac						541
Phe Ile Ser Phe Leu Leu Leu Leu Thr Asp Leu Leu Leu Thr Gly Asn						
	145		150		155	
cct gcc tgt ggg ctc aaa ctg agc gcc ttt gct gct gtt tcc tct gtc						589
Pro Ala Cys Gly Leu Lys Leu Ser Ala Phe Ala Ala Val Ser Ser Val						
	160		165		170	
ctg tca ggt ctc ctg ggg atg gtg gcc cac atg atg tat tca caa gtc						637
Leu Ser Gly Leu Leu Gly Met Val Ala His Met Met Tyr Ser Gln Val						
	175		180		185	
ttc caa gcg act gtc aac ttg ggt cca gaa gac tgg aga cca cat gtt						685
Phe Gln Ala Thr Val Asn Leu Gly Pro Glu Asp Trp Arg Pro His Val						
	190		195		200	205
tgg aat tat ggc tgg gcc ttc tac atg gcc tgg ctc tcc ttc acc tgc						733
Trp Asn Tyr Gly Trp Ala Phe Tyr Met Ala Trp Leu Ser Phe Thr Cys						
	210		215		220	
tgc atg gcg tgc gct gtc acc acc ttc aac acg tac acc agg atg gtg						781
Cys Met Ala Ser Ala Val Thr Thr Phe Asn Thr Tyr Thr Arg Met Val						
	225		230		235	
ctg gag ttc aag tgc aag cat agt aag agc ttc aag gaa aac ccg aac						829
Leu Glu Phe Lys Cys Lys His Ser Lys Ser Phe Lys Glu Asn Pro Asn						
	240		245		250	
tgc cta cca cat cac cat cag tgt ttc cct cgg cgg ctg tca agt gca						877
Cys Leu Pro His His His Gln Cys Phe Pro Arg Arg Leu Ser Ser Ala						
	255		260		265	
gcc ccc acc gtg ggt cct ttg acc agc tac cac cag tat cat aat cag						925
Ala Pro Thr Val Gly Pro Leu Thr Ser Tyr His Gln Tyr His Asn Gln						
	270		275		280	285
ccc atc cac tct gtc tct gag gga gtc gac ttc tac tcc gag ctg cgg						973
Pro Ile His Ser Val Ser Glu Gly Val Asp Phe Tyr Ser Glu Leu Arg						
	290		295		300	
aac aag gga ttt caa aga ggg gcc agc cag gag ctg aaa gaa gca gtt						1021
Asn Lys Gly Phe Gln Arg Gly Ala Ser Gln Glu Leu Lys Glu Ala Val						
	305		310		315	
agg tca tct gta gag gaa gag cag tgt taggagttaa gcgggtttgg gg						1070
Arg Ser Ser Val Glu Glu Glu Gln Cys						
	320		325			
agtaggcttg agccctacct tacacgtctg ctgattatca acatgtgctt aagcc						1125

<210> 20

<211> 1734

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (40)...(1014)

<400> 20

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                                     Met Ala Ala Ala Ala
                                     1           5
ccg gag aac ggc cgc gca tgc gcg ccc cgg ctg ctt ctg ctc ttt ctg      102
Pro Gly Asn Gly Arg Ala Ser Ala Pro Arg Leu Leu Leu Leu Phe Leu
                                     10           15           20
ggt ccg ctg ctg tgg gcc ccg gct gcg gtc cgg gcc ggc cca gat gaa      150
Val Pro Leu Leu Trp Ala Pro Ala Ala Val Arg Ala Gly Pro Asp Glu
                                     25           30           35
gac ctt agc cac cgg aac aaa gaa ccg ccg gcg ccg gcc cag cag ctg      198
Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala Pro Ala Gln Gln Leu
                                     40           45           50
cag ccg cag cct gtg gct gtg cag ggc ccc gag ccg gcc cgg gtc gag      246
Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu Pro Ala Arg Val Glu
                                     55           60           65
aaa ata ttt aca cca gca gct cca gtt cat acc aat aaa gaa gat cct      294
Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr Asn Lys Glu Asp Pro
                                     70           75           80           85
gct acc caa act aat ttg gga ttt atc cat gca ttt gtc gct gcc ata      342
Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala Phe Val Ala Ala Ile
                                     90           95           100
tca gtt att att gta tct gaa ttg ggt gat aag aca ttt ttt ata gca      390
Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys Thr Phe Phe Ile Ala
                                     105           110           115
gcc atc atg gca atg cgc tat aac cgc ctg acc gtg ctg gct ggt gca      438
Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala
                                     120           125           130
atg ctt gcc ttg gga cta atg aca tgc ttg tca gtt ttg ttt ggc tat      486
Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly Tyr
                                     135           140           145
gcc acc aca gtc atc ccc agg gtc tat aca tac tat gtt tca act gta      534
Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr Thr Val Ser Thr Val
                                     150           155           160           165
tta ttt gcc att ttt ggc att aga atg ctt cgg gaa ggc tta aag atg      582
Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg Glu Gly Leu Lys Met
                                     170           175           180
agc cct gat gag ggt caa gag gaa ctg gaa gaa gtt caa gct gaa tta      630
Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu Val Gln Ala Glu Leu
                                     185           190           195
aag aag aaa gat gaa gaa ttt caa cga acc aaa ctt tta aat gga ccg      678
Lys Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys Leu Leu Asn Gly Pro
                                     200           205           210
gga gat gtt gaa acg ggt aca agc ata aca gta cct cag aaa aag tgg      726
Gly Asp Val Glu Thr Gly Thr Ser Ile Thr Val Pro Gln Lys Lys Trp
                                     215           220           225
ttg cat ttt att tca ccc att ttt gtt caa gct ctt aca tta aca ttc      774
Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala Leu Thr Leu Thr Phe
                                     230           235           240           245
tta gca gaa tgg ggt gat cgc tct caa cta act aca att gta ttg gca      822
Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr Thr Ile Val Leu Ala
                                     250           255           260
gct aga gag gac ccc tat ggt gta gcc gtg ggt gga act gtg ggg cac      870
Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly Gly Thr Val Gly His
                                     265           270           275
tgc ctg tgc acg gga ttg gca gta att gga gga aga atg ata gca cag      918
Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly Arg Met Ile Ala Gln
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280	285	290	
aaa atc tct gtc aga act gtg aca atc ata aga ggc atc gtt ttt ttg			966
Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly Gly Ile Val Phe Leu			
295	300	305	
gcg ttt gca ttt tct gca cta ttt ata agc cct gat tct ggt ttt			1011
Ala Phe Ala Phe Ser Ala Leu Phe Ile Ser Pro Asp Ser Gly Phe			
310	315	320	
taacgctgt ttgttcatct atatttagtt taaaataggt agtattatct ttctgtacat			1070
agtgtacatt acaactaaaa gtgatggaaa aatactgtat ttgttagcac tgattttgtg			1130
agtttgaccc attattatgt ctgagatata atcattgatt ctatttgtaa caaggagttt			1190
taaaagaaac ctgacttcta agtgtgggtt tttcttctct ccaacataat tatgttaata			1250
tggtctctcat ttttcttttg gtgcagaacc gttgtgcagt ggggtctacc atgcaatttt			1310
ctttcagcac tgaccocctt ttaaggaata caaattttct ccttcatcac ttaggtgttt			1370
taagatgttt accttaaagt ttttcttggg gaaagaatga attaatctct atttcttaaa			1430
acatttccct gagccagtaa acagtagttt aatcattggt cttttcaaaa ctaggtgttt			1490
aaaaaaagag acatatatga tattgctgtt atatcaataa catggcacia caagaactgt			1550
ctgccagggtc attcttccctc tttttttttt aattgggtag gacaccaat ataaaaacag			1610
tcaatatttg acaatgtgga attacaaat taaaagagaa tactatgaat gtattcatat			1670
tttttctata ttgaataaac aatgtaacat agataacaat ataaataaaa gtggtatgac			1730
cagt			1734

<210> 21  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (98)...(559)

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cttcggcccc acacgaacag cagagagggg cagcagg atg aat gtg ggc aca	112
Met Asn Val Gly Thr	
1 5	
gcg cac agc gag gtg aac ccc aac acg cgg gtg atg aac agc cgt ggc	160
Ala His Ser Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly	
10 15 20	
atc tgg ctc tcc tac gtg ctg gcc atc ggt ctc ctc cac atc gtg ctg	208
Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu Leu His Ile Val Leu	
25 30 35	
ctg agc atc ccg ttt gtg agt gtc cct gtc gtc tgg acc ctc acc aac	256
Leu Ser Ile Pro Phe Val Ser Val Pro Val Val Trp Thr Leu Thr Asn	
40 45 50	
ctc att cac aac atg ggc atg tat atc ttc ctg cac acg gtg aag ggg	304
Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu His Thr Val Lys Gly	
55 60 65	
aca ccc ttt gag acc ccg gac cag ggc aag gcg agg ctg cta acc cac	352
Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His	
70 75 80 85	
tgg gag cag atg gat tat ggg gtc cag ttc acg gcc tct cgg aag ttc	400
Trp Glu Gln Met Asp Tyr Gly Val Gln Phe Thr Ala Ser Arg Lys Phe	
90 95 100	
ttg acc atc aca ccc atc gtg ctg tac ttc ctc acc agc ttc tac act	448
Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu Thr Ser Phe Tyr Thr	
105 110 115	
aag tac gac cag atc cat ttt gtg ctc aac acc gtg tcc ctg atg agc	496
Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr Val Ser Leu Met Ser	
120 125 130	
gtg ctt atc ccc aag ctg ccc cag ctc cac gga gtc cgg att ttt gga	544

Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly Val Arg Ile Phe Gly  
135 140 145  
atc aat aag tac tgagagtga gcccttccc ctgccaggg tggcagggga gggg 600  
Ile Asn Lys Tyr  
150  
tagggtaaaa ggcattgtgt gcaacactga agacagaaag aagaagcctc tggacactgc 660  
cagagatggg gggttagcct ctggcctaata tccccccctc gcttccccca gtagccaact 720  
tggagtagct tgtagtgggg ttggggtagg ccccttgggc tctgaccttt tctgaatttt 780  
ttgatctttt ccttttgcct tttgaataga gactccatgg agttgggtcat ggaatgggct 840  
gggctccttg gctgaacatg gaccacgcag ttgcgcacagg aggccagggg aaaaaccctt 900  
gctcacttgt ttgccctcag gcagccaaag cactttaacc cctgcatagg gagcagaggg 960  
cggtagcggt tctggattgt ttcactgtga ttcttaggtt ttttcgatgc cacgcagtgt 1020  
  
gtgctttttgt gtatggaagc aagtgtggga tgggtctttg cctttctggg tagggagctg 1080  
tctaatacaa gtcccaggct tttggcagct tctctgcaac ccaccgtggg tcttggttgg 1140  
gagtggggag ggtcagggtt gggaaagatg gggtagagtg tagatggctt gggtccagag 1200  
gtgagggggc cagggtctgt gccatcctgg cctggtggag gttggggagc tgtaggagag 1260  
ctagtgaagtc gagacttaga agaattggggc cacatagcag cagaggactg gtgtaaggga 1320  
  
gggaggggta gggacagaag ctagacccaa tctccttttg gatgtgggca gggaggggaag 1380  
caggcttgga ggggttaattt acccacagaa tgtgatagta ataggggagg gaggctgctg 1440  
tgggtttaac tcttgggttg gctgttgggt agacagggtg ggaaaaggcc cgtgagtcac 1500  
tgtaagcaca ggtccaactt ggccctgact cctgcggggg tatggggaag ctgtgacaga 1560  
aacgatgggt gctgtgggtc tctgcaggcc ctcacccctt aacttctca tacagactgg 1620  
cactgggcag ggcctctcat gtggcagcca catgtggcgt tgtgaggcca cccatgttg 1680  
ggtctgtggt gagagtcttg taggatccct gctcaagcag cacagaggaa ggggcaagac 1740  
gtggcctgta ggcactgttt cagcctgcag agaagaaagt gaggcggga gcctgagcct 1800  
gggctggagc cttctccctt cccagtttg actaggggca gtgttaattt tgaaaagggtg 1860  
tgggtccctg tgtcctcttc caggggtcca agggaacagg agaggtcact gggcctgttt 1920  
tctccctcct gacctgcat ctcccacccc gtgtatcata gggaactttc accttaaaat 1980  
ctttctaagc aaagtgtgaa taggattttt actccctttg tacagtattc tgagaaacgc 2040  
aaataaaagg gcaacatgtt tctg 2064

<210> 22  
<211> 570  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (28)...(489)

<400> 22  
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Met Asn Val Gly Val Ala His Ser  
1 5  
gaa gta aac ccc aac acc cga gtg atg aat agc cga ggc atc tgg ctg 99  
Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly Ile Trp Leu  
10 15 20  
gcc tac atc atc ttg gta gga ttg ctg cat atg gtt cta ctc agc atc 147  
Ala Tyr Ile Ile Leu Val Gly Leu Leu His Met Val Leu Leu Ser Ile  
25 30 35 40  
ccc ttc ttc agc att cct gtt gtc tgg acc ctg acc aac gtc atc cat 195  
Pro Phe Phe Ser Ile Pro Val Val Trp Thr Leu Thr Asn Val Ile His  
45 50 55  
aac ctg gct acg tat gtc ttc ctt cat acg gtg aaa ggg aca ccc ttt 243

Asn	Leu	Ala	Thr	Tyr	Val	Phe	Leu	His	Thr	Val	Lys	Gly	Thr	Pro	Phe	
			60					65					70			
gag	act	cct	gac	caa	gga	aag	gct	cgg	cta	ctg	aca	cac	tg	gag	caa	291
Glu	Thr	Pro	Asp	Gln	Gly	Lys	Ala	Arg	Leu	Leu	Thr	His	Trp	Glu	Gln	
			75				80					85				
atg	gac	tat	ggg	ctc	cag	ttt	acc	tct	tcc	cgc	aag	ttc	ctc	agc	atc	339
Met	Asp	Tyr	Gly	Leu	Gln	Phe	Thr	Ser	Ser	Arg	Lys	Phe	Leu	Ser	Ile	
			90			95					100					
tct	cct	att	gtg	ctc	tat	ctc	ctg	gcc	agc	ttc	tat	acc	aag	tat	gat	387
Ser	Pro	Ile	Val	Leu	Tyr	Leu	Leu	Ala	Ser	Phe	Tyr	Thr	Lys	Tyr	Asp	
105					110					115					120	
gct	gcg	cac	ttc	ctc	atc	aac	aca	gcc	tca	ttg	cta	agt	gta	ctg	ctg	435
Ala	Ala	His	Phe	Leu	Ile	Asn	Thr	Ala	Ser	Leu	Leu	Ser	Val	Leu	Leu	
				125					130					135		
ccg	aag	ttg	ccc	cag	ttc	cat	ggg	gtt	cgt	gtc	ttt	ggc	atc	aac	aaa	483
Pro	Lys	Leu	Pro	Gln	Phe	His	Gly	Val	Arg	Val	Phe	Gly	Ile	Asn	Lys	
			140					145				150				
tac	tgag	ggatggg	ttt	tg	ggacagct	ccatggg	cat	ggggaagg	ca	ctgaaacaga						540
Tyr																

ggactataaa acatccttct cttattctcc 570

<210> 23  
 <211> 1161  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (278)... (880)

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gaacttaatc tttcatgaga aactgaggat agagatgtca ataagcagcc actgtttcca	180
cctccccacc tgaagagcta ggaggacaac tacaaagagc ctgactgcct tctcggaatg	240
aggagagagg aaaacagcaa cagtatcagt tttcaag atg gca gca tct atg	292
	Met Ala Ala Ser Met
	1 5
cat ggt cag ccc agt cct tct cta gaa gat gca aaa ctc aga aga cca	340
His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala Lys Leu Arg Arg Pro	
	10 15 20
atg gtc ata gaa atc ata gaa aaa aat ttt gac tat ctt aga aaa gaa	388
Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp Tyr Leu Arg Lys Glu	
	25 30 35
atg aca caa aat ata tat caa atg gcg aca ttt gga aca aca gct ggt	436
Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe Gly Thr Thr Ala Gly	
	40 45 50
ttc tct gga ata ttc tca aac ttc ctg ttc aga cgc tgc ttc aag gtt	484
Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg Arg Cys Phe Lys Val	
	55 60 65
aaa cat gat gct ttg aag aca tat gca tca ttg gct aca ctt cca ttt	532
Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu Ala Thr Leu Pro Phe	
	70 75 80 85
ttg tct act gtt gtt act gac aag ctt ttt gta att gat gct ttg tat	580
Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val Ile Asp Ala Leu Tyr	
	90 95 100
tca gat aat ata agc aag gaa aac tgt gtt ttc aga agc tca ctg att	628
Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe Arg Ser Ser Leu Ile	
	105 110 115



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ggc ata gtt tgt ggt gtt ttc tat ccc agt tct ttg gct ttt act aaa 676
Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser Leu Ala Phe Thr Lys
120 125 130
aat gga cgc ctg gca acc aag tat cat acc gtt cca ctg cca cca aaa 724
Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val Pro Leu Pro Pro Lys
135 140 145
gga agg gtt tta atc cat tgg atg acg ctt tgt caa aca caa atg aaa 772
Gly Arg Val Leu Ile His Trp Met Thr Leu Cys Gln Thr Gln Met Lys
150 155 160 165
tta atg gcg att cct cta gtc ttt cag att atg ttt gga ata tta aat 820
Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met Phe Gly Ile Leu Asn
170 175 180
ggg cta tac cat tat gca gta ttt gaa gag aca ctt gag aaa act ata 868
Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr Leu Glu Lys Thr Ile
185 190 195
cat gaa gag taacacaaaaa aatgaatggg tgctaactta gcaaaatgaa gtt 920
His Glu Glu
200
tctataaaga ggactcaggc attgctgaaa gagttaaaag taactgtgaa caaataattt 980
gttctgtgcc ttttgccctgg tatatagcaa atactcaaaa agtattcaat aattcaatca 1040

ataaatataa gtttcatctt acacgtaaga tacagggtctt atctcctgat ggtgtgtcca 1100

ttttgcctgg tatataacag ataataaata tccagtgtca ataaatgtaa caataaaagt 1160
t 1161

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<210> 24  
<211> 823  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (58)...(627)

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atg agg ctg tca ctg cca ctg ctg ctg ctg ctg gga gcc tgg gcc 105
Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Leu Gly Ala Trp Ala
1 5 10 15
atc cca ggg ggc ctc ggg gac agg gcg cca ctc aca gcc aca gcc cca 153
Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro
20 25 30
caa ctg gat gat gag gag atg tac tca gcc cac atg ccc gct cac ctg 201
Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu
35 40 45
cgc tgt gat gcc tgc aga gct gtg gct tac cag atg tgg caa aat ctg 249
Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu
50 55 60
gca aag gca gag acc aaa ctt cat acc tca aac tct ggg ggg cgg cgg 297
Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg
65 70 75 80
gag ctg agc gag ttg gtc tac acg gat gtc ctg gac cgg agc tgc tcc 345
Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Ser Cys Ser
85 90 95
cgg aac tgg cag gac tac gga gtt cga gaa gtg gac caa gtg aaa cgt 393
Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg
100 105 110
ctc aca ggc cca gga ctt agc gag ggg cca gag cca agc atc agc gtg 441
Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val

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	115		120		125	
atg gtc aca ggg ggc ccc tgg cct acc agg ctc tcc agg aca tgt ttg						489
Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu						
130		135		140		
cac tac ttg ggg gag ttt gga gaa gac cag atc tat gaa gcc cac caa						537
His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln						
145		150		155		160
caa ggc cga ggg gct ctg gag gca ttg cta tgt ggg gga ccc cag ggg						585
Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly						
	165		170		175	
gcc tgc tca gag aag gtg tca gcc aca aga gaa gag ctc tagtcc						630
Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu						
	180		185			
tggaactctac cctcctctga aagaagctgg ggcttgctct gacgggtctcc actcccgtct						690
gcaggcagcc aggagggcag gaagcccttg ctctgtgctg ccatacctgcc tccctcctcc						750
agcctcaggg cactcggggc tgggtgggag tcaacgcctt cccctctgga ctcaaataaa						810
accagtgac ctc						823